The Word

We’re going to submit samples to the Clock Foundation.

We have three categories of samples:

1. Extracted, enough DNA
2. Extracted, problematic amount of DNA (low or negative)
3. Non-extracted

They each need to be dealt with in different ways before sending them in.

1. Extracted, enough DNA
   1. Re-quant
   2. Moved to final plate position
2. Extracted, problematic amount
   1. Re-quant
   2. Move to final plate position
3. Non-extracted
   1. Extract
   2. quant

Considerations

1. Limit freeze-thaw
2. If quanting shows that value isn’t enough what do we do?
   1. Take it out of well, leave well empty
   2. Take all out of wells, consolidate leftovers into new well

Order of operations upon return

1. SPRI bead test
   1. My beads, Manny’s beads, thermo DNA ladder
2. Extraction practice run
   1. Quant with qubit
3. Extract all
4. Compile all onto plates
5. Plate reader quant all
6. Move into final positions/remove bad ones based on quant

* There are still a few samples missing. Those are the samples that are not labeled ‘yes’ in the NotExtracted tab of the FinalSample excel spreadsheet. We need to figure out what to do about those.
* For samples that we are confident are just too low quantity, what do we do? Maybe they’re just a bust?